

GenCore version 5.1.3
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M protein - protein search, using sw model

Run on: January 13, 2003, 15:56:17 : Search time 13 612 Seconds
(without alignments)
1604.450 Million cell updates/sec

Title: US-09-234-733a-5

Perfect score: 1108
Sequence: 1 NQIYVQGFENEDNVIQGF.....VAQYGEIYVLEALNTAQ 228

Scoring table: BLOSUM62
Gapop 12.0 , Gapext 0.5

Searched: 281224 seqs, 36134422 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 90%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 731*
1: PIR1*
2: PIR2*
3: PIR3*
4: PIR4*

Pired. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match length	DB ID	Description
.....					

No matches found

Search completed: January 13, 2003, 15:59:41
Job time: 13.6612 secs

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CM protein - protein search, using SW model

Run on: January 13, 2003, 10:04:50, Search time 9.6036 Seconds
(without alignments)
1180.455 Million cell updates/sec

Title: US-09-234-733a-5

Protein score: 1118
Sequence: I M Q I W V G F T D N G F T W I S L Y F V A G Y E L I W V L E A N T A L S 228

Scoring table: BLOSUM62
Gapop 11.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post processing: Minimum Match 93%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt 401*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
No matches found					

Search completed: January 13, 2003, 15:59:05
Job time: 8.0926 secs

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QM protein - protein search, using SW model

Run on: January 13, 2003, 15:57:48 : Search time 8.99174 Seconds
(without alignments)
\$52.360 Million cell updates/sec

Title: US-09-234 733a-2

Perfect score: 1292
Sequence: 1 MEFFR1VITGSLACITFS.....VAGVGEIRVLGSLTALQ 206

Scoring table: BLOSUM62
Gapop 15.0 , Gapext 0.5

Query: 11974 seqs, 194057 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 3
Maximum DB seq length: 200000000

Post processing: Minimum Match 93%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA*

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1: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
2: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
3: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
4: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
5: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
6: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
7: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
8: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
9: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
10: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
11: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
12: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
13: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*
14: /cgn2_6/f/.../Fufaa/FCT_NEW_PUB.pep.*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
No matches found							

Search completed: January 13, 2003, 16:00:38
Run time: 8.99174 secs

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CM protein protein search, using SW model

Run on: January 13, 2003, 15:56:17, Search time 15.3388 Seconds
(without alignments)
1604.450 Million cell updates/sec

Title: US-09-234-733a-2
Perfect score: 1242
Sequence: 1 MEKKKLYTSSIGITTFSS.....VAQVDCEIKVLEALNTALD 256

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Sequences: 281224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 3
Maximum DB seq length: 200000000

Post processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 731*
1: pir1*
2: pir2*
3: pir3*
4: pir4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	ID	Description
No matches found					

Search completed: January 13, 2003, 15:59:41
Job time: 16.3388 secs

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SW protein - protein search, using sw model

Run on: January 13, 2003, 15:53:17 : Search time 9.99174 seconds
(without alignments)
1180.855 Million cell updates/sec

Title: US-09-234-733A.2
Perfect score: 1252
Sequence: 1 MEFPRLLVLTLSIAAILTS.....VWVQGLRVLQSEANILAQ 256

Scoring table: BLOSUM62
Gapop 13.0, Gapext 7.5

Searched: 112802 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 0

Minimum 28 seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 90%
Maximum Match 100%
Listing first 45 summaries

Database: 1 SwissProt_401*

Note: No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
Description					
No matches found					

Search completed: January 13, 2003, 15:58:05
Job time: 9.99174 secs